

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/552,857  
Source: pu5/10  
Date Processed by STIC: 10/24/05

***ENTERED***



PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/552,857

DATE: 10/24/2005

TIME: 10:50:34

Input Set : A:\sequence.txt

Output Set: N:\CRF4\10242005\J552857.raw

4 <110> APPLICANT: Agriculture Victoria Services Pty Ltd  
 5       AgResearch Limited  
 6       Spangenberg, German  
 7       Emmerling, Michael  
 8       Simmonds, Jason  
 9       Winkworth, Amanda  
 10      Panter, Stephen  
 12 <120> TITLE OF INVENTION: Chlacone synthase dihydroflavonol-4-reductase and  
 13        leucoanthocyanidine reductase for clover, medic  
 14        rygrass or fescue  
 17 <130> FILE REFERENCE: FREE.P-007  
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/552,857  
 C--> 20 <141> CURRENT FILING DATE: 2005-10-14  
 20 <150> PRIOR APPLICATION NUMBER: 2003901797  
 21 <151> PRIOR FILING DATE: 2003-04-14  
 24 <150> PRIOR APPLICATION NUMBER: 2003904369  
 25 <151> PRIOR FILING DATE: 2003-08-14  
 28 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/00494  
 W--> 29 <151> PRIOR FILING DATE: 2004-4-14  
 32 <160> NUMBER OF SEQ ID NOS: 77  
 35 <170> SOFTWARE: PatentIn version 3.2  
 38 <210> SEQ ID NO: 1  
 39 <211> LENGTH: 1447  
 40 <212> TYPE: DNA  
 41 <213> ORGANISM: Trifolium repens  
 44 <400> SEQUENCE: 1

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48	acgcattatta tatatatata tatatagtct ataattgaaa gaaactgcTA aagatattat		120
51	taagatatgg tgagttagc tggaaattcgc aaggctcaga gggctgaagg ccctgcAAC		180
54	atttggCCA ttggcaactgc aaatccacca aaccgtgttG agcagagcac atatcctgtat		240
57	ttotacttca aaattacaaa cagtgagcac aagactgagc tcaaagagaa gttccaaAC		300
60	atgtgtgaca aatccatgtat caagagcaga tacatgtatc taacagaAGA gatttgaaa		360
63	gaaaatccta gtctttgtGA atacatggca ctttcattgg atgctaggca agacatggTG		420
66	gtggttgagg tacctagact tggaaaggAG gctgcagtca aggccattaa agaatgggGT		480
69	caaccaaAGT caaagattac tcacttaatc tttgcacca caagtggTGT tgacatgcCT		540
72	gggtctgatt accaactcac aaaactctta ggtcttcGCC catatgtgaa aaggatata		600
75	atgtaccaac aaggTTGTT tgcaggaggc acgggtctc gtttggAAA agatttggCC		660
78	gagaacaaca aagggtctcg tggcttagtt gtttggctG aagtccACCGC agtcacattt		720
81	cgccggccccca gtgatactca ctggacAGT cttgtggac aagcatttt tggagatggA		780
84	gccgctgcac taattttgg tctgatcca gtcctgAAA ttgagAAACC aatatttgAG		840
87	atggTTGGA ctgcacAAAC aattgtctca gacagtGAAG gtgcCATTGA tggTCatTT		900
90	cgtgaagctg ggctAACATT tcattttctt aaagatgttc ctgggattgt atcaaAGAAC		960
93	attaataaaAG cattgggtGA ggctttccaa ccatttagAA tttctgacta caactcaatC		1020

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96 ttttggattg cacaccggg tggacctgca attcttgatc aagtagaaaca aaagcttagcc 1080  
 99 ttgaagcccg aaaagatgag ggccacgagg gaagttctaa gtgaatatgg aaacatgtca 1140  
 102 agcgcatgtg tattttcat cttagatgag atgcggaga aatcggtca aaatggactt 1200  
 105 aagacaaactg gagaaggact tgattgggt gtgtgttcg gcttcggacc aggacttacc 1260  
 108 attgaaaccg ttgttcttcg tagcgtggct atataagatg tgtgattttt 1320  
 111 tgattactt ttaatcttcg tgccttgaat ttgcattaa gaataaataa atatatctt 1380  
 114 tgataaaaaa aaaaaaaaaa aaaaaaaaaa aagtactctg cgttgttacc actgcttaat 1440  
 117 cgaattc 1447  
 121 <210> SEQ ID NO: 2  
 122 <211> LENGTH: 389  
 123 <212> TYPE: PRT  
 124 <213> ORGANISM: Trifolium repens  
 127 <400> SEQUENCE: 2  
 130 Met Val Ser Val Ala Glu Ile Arg Lys Ala Gln Arg Ala Glu Gly Pro  
 131 1 5 10 15  
 135 Ala Thr Ile Leu Ala Ile Gly Thr Ala Asn Pro Pro Asn Arg Val Glu  
 136 20 25 30  
 140 Gln Ser Thr Tyr Pro Asp Phe Tyr Phe Lys Ile Thr Asn Ser Glu His  
 141 35 40 45  
 145 Lys Thr Glu Leu Lys Glu Lys Phe Gln Arg Met Cys Asp Lys Ser Met  
 146 50 55 60  
 150 Ile Lys Ser Arg Tyr Met Tyr Leu Thr Glu Glu Ile Leu Lys Glu Asn  
 151 65 70 75 80  
 155 Pro Ser Leu Cys Glu Tyr Met Ala Pro Ser Leu Asp Ala Arg Gln Asp  
 156 85 90 95  
 160 Met Val Val Val Glu Val Pro Arg Leu Gly Lys Glu Ala Ala Val Lys  
 161 100 105 110  
 165 Ala Ile Lys Glu Trp Gly Gln Pro Lys Ser Lys Ile Thr His Leu Ile  
 166 115 120 125  
 170 Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp Tyr Gln Leu  
 171 130 135 140  
 175 Thr Lys Leu Leu Gly Leu Arg Pro Tyr Val Lys Arg Tyr Met Met Tyr  
 176 145 150 155 160  
 180 Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu Ala Lys Asp  
 181 165 170 175  
 185 Leu Ala Glu Asn Asn Lys Gly Ala Arg Val Leu Val Val Cys Ser Glu  
 186 180 185 190  
 190 Val Thr Ala Val Thr Phe Arg Gly Pro Ser Asp Thr His Leu Asp Ser  
 191 195 200 205  
 195 Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala Leu Ile Val  
 196 210 215 220  
 200 Gly Ser Asp Pro Val Pro Glu Ile Glu Lys Pro Ile Phe Glu Met Val  
 201 225 230 235 240  
 205 Trp Thr Ala Gln Thr Ile Ala Pro Asp Ser Glu Gly Ala Ile Asp Gly  
 206 245 250 255  
 210 His Leu Arg Glu Ala Gly Leu Thr Phe His Leu Leu Lys Asp Val Pro  
 211 260 265 270  
 215 Gly Ile Val Ser Lys Asn Ile Asn Lys Ala Leu Val Glu Ala Phe Gln  
 216 275 280 285

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220 Pro Leu Gly Ile Ser Asp Tyr Asn Ser Ile Phe Trp Ile Ala His Pro  
 221 290 295 300  
 225 Gly Gly Pro Ala Ile Leu Asp Gln Val Glu Gln Lys Leu Ala Leu Lys  
 226 305 310 315 320  
 230 Pro Glu Lys Met Arg Ala Thr Arg Glu Val Leu Ser Glu Tyr Gly Asn  
 231 325 330 335  
 235 Met Ser Ser Ala Cys Val Leu Phe Ile Leu Asp Glu Met Arg Lys Lys  
 236 340 345 350  
 240 Ser Ala Gln Asn Gly Leu Lys Thr Thr Gly Glu Gly Leu Asp Trp Gly  
 241 355 360 365  
 245 Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Ile Glu Thr Val Val Leu  
 246 370 375 380

250 Arg Ser Val Ala Ile

251 385

255 &lt;210&gt; SEQ ID NO: 3

256 &lt;211&gt; LENGTH: 2394

257 &lt;212&gt; TYPE: DNA

258 &lt;213&gt; ORGANISM: Trifolium repens

261 &lt;400&gt; SEQUENCE: 3

262	gaattcgtt	aaggcgttgg	aacaacgcag	agtacgcggg	gattcaatct	gttgtgcata	60
265	aaatttcactc	attgcata	aaaccataca	catttgatct	tgcaaagaag	aaatatggga	120
268	gacgaaggta	tagtgagagg	tgtcacaaag	cagacaaccc	ctgggaaggc	tactatattg	180
271	gctcttggca	aggcattccc	tcaccaactt	gtgatgcaag	agtgttagt	tgatggttat	240
274	tttagggaca	ctaattgtga	caatcctgaa	cttaagcaga	aacttgctag	actttgtaa	300
277	acaaccacgg	taaaaacaag	gtatgttgg	atgaatgagg	agataactaaa	gaaatatcca	360
280	gaacttgg	tcgaaggcgc	ctcaactgt	aaacaacgtt	tagagatatg	taatgaggca	420
283	gtAACACAAA	TGGCAATTGA	AGCTTCCAA	GTTCGCCTAA	AGAATTGGGG	TAGATCCTTA	480
286	TCGGACATAA	CTCATGTGGT	TTATGTTCA	TCTAGTGAAG	CTAGATTACC	CGGTGGTGCAC	540
289	CTATACTTGT	CAAAAGGACT	AGGACTAAAC	CCTAAAATT	AAAGAACCAT	GCTCTATTTC	600
292	TCTGGATGCT	CGGGAGGC	GTAGCCGC	CGCGTTGC	AAAGACGTAGC	TGAGAACAAAC	660
295	CCTGGAAAGTA	GAGTTTGCT	TGCTACTTCG	GAAACTACAA	TTATTGGATT	CAAGCCACCA	720
298	AGTGTGATA	GACCTTATGA	TCTTGTGTT	GTGGCACTCT	TTGGAGATGG	TGCTGGTGC	780
301	ATGATAATTG	GTCAGACCC	GGTATTGAA	ACTGAGACAC	CATTGTTGA	GCTGCATACT	840
304	TCAAGCTCAGG	AGTTTATAACC	AGACACCGAG	AAGAAAATTG	ATGGGCGCT	GACGGAGGAG	900
307	GGCATAAGT	TCAACACTAGC	AAGGGAACCT	CCGCAAGATAA	TGCAAGACAA	TGTGAGGGA	960
310	TTCCTGTAATA	AACTAATTGA	TGTTGTTGGG	TTGGAGAATA	AGGAGTACAA	TAAGTTGTT	1020
313	TGGGCTGTGC	ATCCAGGTGG	GCCTGCGATA	TTGAATCGCG	TGGAGAAAGCG	GCTTGAGTTG	1080
316	TCGCCGAGA	AGCTGAATGC	TAGTAGAAAA	GCTCTAATGG	ATTATGGAAA	TGCTAGCAGC	1140
319	AATACTATTG	TTTATGTGCT	GGAATATATG	CTAGAAGAGG	AAAAGAAAGAT	AAAAAGGCG	1200
322	GGTGGAGGAG	ATTCTGAATG	GGGATTGATA	CTTGCTTTG	GACCTGGAAT	TACTTTGAG	1260
325	GGGATTCTAG	CAAGGAACCT	GTGTGCATGA	AGTCCTATAC	AATTGTGATG	CATGACTTAT	1320
328	ACTCTTATT	CTACTAATT	TTATATTAG	CAAATTCA	ACTTTAAGT	AATGATTAA	1380
331	TGAAGAACAC	TTAGTAGATA	TGACTTTAT	TCACCTCAA	AGCAAGTTA	TGATCCTAA	1440
334	ACATGGTAGA	ACTTGAGCAT	GTGGAATAGT	TGTAACAAAA	ACTCTAAC	AATAGAGACT	1500
337	TTATGTTAGTA	AAAGCATT	CCAGACATGA	AAATAATGG	TACCTCAGAA	CATAAAATAT	1560
340	ATTTAGCTAT	CTTCATCCC	CAACTTACA	CATCCACCAA	GGTACAGAA	AAGCATATGT	1620
343	CAACACAAAAA	TGTACTCTAA	GTCTAACATG	AGTAACAAA	CATGATGCC	GATTAAGTTA	1680
346	AAAGAAAAGA	AAATCTGAGG	GCTAGATCT	TCAATCACAC	CACTCCAGAG	GGAAGGCGTA	1740
349	GAACAAGCTG	TCCGCCGAAA	ACACTGCAAT	TCAATAAATA	TCATTAGGAC	AACAGTGCAG	1800

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352 agtcatgcgg gaaatgtctt aagtcaactgt actaaaaata taggattata ttatgaacta 1860  
355 tactaacctt ttcacataat agtaacagaa atcagctaag atgaatgtct ggacaattc 1920  
358 ttagataaga accatgacgg ccataagcca taccggcaagg caaccaataa atgtccacgg 1980  
361 gtagtcaaca cctgtgcaa gaaatagtaa gttatttagga gatgtgcgg ttagaaattc 2040  
364 aagctacaca acaaaggag gccagaacaa cagcaatctt gtaaccagat gacaacaata 2100  
367 aaatgtaaac ttaaagagac cgaacacaca aacattgcaa ctcagatgga attgctgcca 2160  
370 tgtaactagt aggagatttggacgtcaa tcagatatt atgcaatac aaggtatgac 2220  
373 cgcctgtctt atttagcat acaacaaacg tacagtgggt ttgtccctct caaaatggca 2280  
376 ggatcttac agcacaatat ttgggggtt catacttata ccataaaaaaa aaaaaaaaaa 2340  
379 aaaaaaaaaaa aaagtactct gcgttggtaa cactgcttaa tcactagtga attc 2394  
383 <210> SEQ ID NO: 4  
384 <211> LENGTH: 391  
385 <212> TYPE: PRT  
386 <213> ORGANISM: Trifolium repens  
389 <400> SEQUENCE: 4  
392 Met Gly Asp Glu Gly Ile Val Arg Gly Val Thr Lys Gln Thr Thr Pro  
393 1 5 10 15  
397 Gly Lys Ala Thr Ile Leu Ala Leu Gly Lys Ala Phe Pro His Gln Leu  
398 20 25 30  
402 Val Met Gln Glu Cys Leu Val Asp Gly Tyr Phe Arg Asp Thr Asn Cys  
403 35 40 45  
407 Asp Asn Pro Glu Leu Lys Gln Lys Leu Ala Arg Leu Cys Lys Thr Thr  
408 50 55 60  
412 Thr Val Lys Thr Arg Tyr Val Val Met Asn Glu Glu Ile Leu Lys Lys  
413 65 70 75 80  
417 Tyr Pro Glu Leu Val Val Glu Gly Ala Ser Thr Val Lys Gln Arg Leu  
418 85 90 95  
422 Glu Ile Cys Asn Glu Ala Val Thr Gln Met Ala Ile Glu Ala Ser Gln  
423 100 105 110  
427 Val Cys Leu Lys Asn Trp Gly Arg Ser Leu Ser Asp Ile Thr His Val  
428 115 120 125  
432 Val Tyr Val Ser Ser Ser Glu Ala Arg Leu Pro Gly Gly Asp Leu Tyr  
433 130 135 140  
437 Leu Ser Lys Gly Leu Gly Leu Asn Pro Lys Ile Gln Arg Thr Met Leu  
438 145 150 155 160  
442 Tyr Phe Ser Gly Cys Ser Gly Gly Val Ala Gly Leu Arg Val Ala Lys  
443 165 170 175  
447 Asp Val Ala Glu Asn Asn Pro Gly Ser Arg Val Leu Leu Ala Thr Ser  
448 180 185 190  
452 Glu Thr Thr Ile Ile Gly Phe Lys Pro Pro Ser Val Asp Arg Pro Tyr  
453 195 200 205  
457 Asp Leu Val Gly Val Ala Leu Phe Gly Asp Gly Ala Gly Ala Met Ile  
458 210 215 220  
462 Ile Gly Ser Asp Pro Val Phe Glu Thr Glu Thr Pro Leu Phe Glu Leu  
463 225 230 235 240  
467 His Thr Ser Ala Gln Glu Phe Ile Pro Asp Thr Glu Lys Lys Ile Asp  
468 245 250 255  
472 Gly Arg Leu Thr Glu Glu Gly Ile Ser Phe Thr Leu Ala Arg Glu Leu  
473 260 265 270

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477 Pro Gln Ile Ile Glu Asp Asn Val Glu Gly Phe Cys Asn Lys Leu Ile  
 478 275 280 285  
 482 Asp Val Val Gly Leu Glu Asn Lys Glu Tyr Asn Lys Leu Phe Trp Ala  
 483 290 295 300  
 487 Val His Pro Gly Gly Pro Ala Ile Leu Asn Arg Val Glu Lys Arg Leu  
 488 305 310 315 320  
 492 Glu Leu Ser Pro Gln Lys Leu Asn Ala Ser Arg Lys Ala Leu Met Asp  
 493 325 330 335  
 497 Tyr Gly Asn Ala Ser Ser Asn Thr Ile Val Tyr Val Leu Glu Tyr Met  
 498 340 345 350  
 502 Leu Glu Glu Glu Lys Lys Ile Lys Lys Ala Gly Gly Asp Ser Glu  
 503 355 360 365  
 507 Trp Gly Leu Ile Leu Ala Phe Gly Pro Gly Ile Thr Phe Glu Gly Ile  
 508 370 375 380  
 512 Leu Ala Arg Asn Leu Cys Ala  
 513 385 390  
 517 <210> SEQ ID NO: 5  
 518 <211> LENGTH: 1653  
 519 <212> TYPE: DNA  
 520 <213> ORGANISM: Trifolium repens  
 523 <400> SEQUENCE: 5  
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 527 ttgtttccat aacacaagaa ctatgtttt cttgaatctt aagaaaaaaat gcctcaagg 120  
 530 gatttgaatg gaagttcctc ggtgaatgga gcacgtgcta gacgtgcctcc tactcagg 180  
 533 aaggcaacga tacttgcatt aggaaaggct ttcccccgc c aggtcctcc tcaagagtgc 240  
 536 ttgggttggaa gattcattcg cgacactaag tgtgacgata cttatattaa ggagaaattg 300  
 539 gagcgtctt gcaaaaacac aactgtgaaa acaagataca cagtaatgtc aaaggagatc 360  
 542 ttagacaact atccagagct agccatagat ggaacacccaa caataaggca aaagcttgaa 420  
 545 atagcaaatc cagcagtagt tgaaatggca acaagagcaa gcaaaaggatg catcaaagaa 480  
 548 tggggaaaggc caccctaaata tattcacacat atatgttatg ttccctcgag cgaaattcgt 540  
 551 ctacccgggt gtgaccttta tcttgcaaat gaactcggt taaaacagcga tgttaatcgc 600  
 554 gtaatgctt atttcctcggt ttgctacggc ggtgtcactg gcttacgtgt cgccaaagac 660  
 557 atcggccgaaa ataaccctgg tagtaggggtt ttactcacaat catccqagac cactattctc 720  
 560 ggttttcgac caccgagtaa agctagacat tatgacctcg ttggcgctgc actttcggt 780  
 563 gatggcgcccg ctgctgcaat aatttggaaaca gaccctatata tgaatcaaga atcaccttc 840  
 566 attggaaatttga accatgcgtt ccaaaaatc ttgcctgata cacaatgtt gattgtgg 900  
 569 agaatcactg aagagggtat taattttaag cttgaaagag accttcctca aaaaatttggaa 960  
 572 gacaatatttga aagaatttttgc caagaaaaattt atggctaaaaa gtgtatgtt ggaattttat 1020  
 575 gacttattttt gggctgttca tcctgggtgg ccagctatac tcaataagctt agaaaaatata 1080  
 578 ctcaaatttga aaagtgtataa attggattgtt agtaggaagg cattaaatggta ttatggaaat 1140  
 581 gttatgttca atactatattt ctatgtgtt ggtttttttt gatggaaatggat 1200  
 584 ggaagtgttca aatggggattt aggattggctt ttggaccagg ggtttttttt tgaaggggttt 1260  
 587 ctccctccgtt gcctttaatc ttgaaataat aattcatatg aaattacttgc tcttaagatt 1320  
 590 gtgtatggaa gatgtatgtt tattggattt atattgtat ggtgttattt taagttgtt 1380  
 593 ttaaaaaaatggaa ttatataataa aagtatgtt taacaattgtt tttttttttt taaaagg 1440  
 596 agtataactat tttaagttctt tgaccataactt gattttttctt ttacacatttt tcatatctaa 1500  
 599 aattgttctt tgatataatc attgttgttata ctgtatataat ataataatcta atttggctgg 1560  
 602 caaaaatggaaa gattttcac cgaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aagtactctg 1620  
 605 cgttggttacc actgcttaat cacttagtggaa ttc 1653

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/24/2005  
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### Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40  
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Seq#:65,66,67,68,69,70,71,72,73,74,75,76,77

**VERIFICATION SUMMARY**

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L:20 M:270 C: Current Application Number differs, Replaced Current Application No

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:29 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD